

IN THE CLAIMS

Please amend the claims as follows:

Claim 1 (Currently Amended): A computer program product embodied on a computer readable medium that executes a method for identifying groups of co-regulated and co-expressed genes, the method comprising:

defining a clustering criterion of data, relating to gene expression that varies with time and/or with the changing of environmental conditions, which is stored in a table;

in function of said clustering criterion, identifying in sub-tables groups of genes that satisfy said clustering criterion;

defining a number of logic filtering criteria of the data of said table;

for each logic filtering criterion, generating a corresponding filtered sub-table containing data of genes having expression values which satisfy said logic filtering criterion;

establishing pair combinations of said sub-tables by clustering and filtering the data of said table with said filtering criteria and by said clustering;

calculating characteristic parameters of the data associated to the groups of genes of each pair combination;

generating for each pair combination a characteristic value in function of the characteristic parameters of the groups of genes by a decision algorithm based on soft computing techniques;

identifying the groups of genes associated with pair combinations whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes involved in a particular cellular process and discarding pair combinations of groups of genes whose characteristic value is smaller than said threshold; and

outputting to a user the group of genes within the pair combinations having characteristic values greater than the threshold in a selected data format.

Claim 2 (Canceled).

Claim 3 (Currently Amended): The computer program product ~~method~~ of claim 1, wherein said decision algorithm is a fuzzy logic algorithm having antecedents and consequents which are defined in function of said parameters.

Claim 4 (Currently Amended): The computer program product ~~method~~ of claim 1, wherein said parameters are chosen from the group consisting of parameters tied to gene expression levels, parameters having a semantic biological meaning, and mixed parameters expressing at the same time a numerical relationship and a semantic meaning.

Claim 5 (Currently Amended): The computer program product ~~method~~ of claim 4, wherein said numeric parameters are chosen from a group consisting of:

absolute values of linear correlation coefficients among data associated to pairs of genes;

absolute values of quadratic correlation coefficients among data associated to pairs of genes;

percentage of genes of the pair combination having a final value of gene expression of which is greater than a respective value of initial gene expression;

percentage of genes of the pair combination having a final value of gene expression of which is smaller than a respective value of initial gene expression;

percentage of genes having values of gene expression which have a same increasing or decreasing time evolution; and

percentage of genes that have a maximum value of gene expression in a same condition; and

wherein said parameters having a semantic biological meaning are chosen from a group consisting of:

percentage of genes that have ontologies in common; and

percentage of genes that have functional domains in common.

Claim 6 (Currently Amended): The computer program product ~~method~~ of claim 1, further comprising discarding combinations among sub-tables constituted by a number of genes smaller than a certain pre-established number, wherein genes that are comprised in both combined sub-tables are considered only once in connection with discarding.

Claim 7 (Currently Amended): The computer program product ~~method~~ of claim 1, wherein said clustering criteria are based on algorithms chosen in a set comprising [[:]] agglomerative hierarchic algorithms, non hierarchic Kmeans algorithms, hierarchic sequential Kmeans, non-hierarchic SOM and not exclusive Fuzzy Clustering.

Claim 8 (Currently Amended): The computer program product ~~method~~ of claim 5, comprising:

calculating correlation coefficients of all pairs of gene sequences of the pair combination;
subdividing an interval from 0 to 1 in five sub-intervals of equal length and assigning to each of said sub-intervals a respective quantized value of correlation;

calculating the percentage of correlation coefficients belonging to each sub-interval;

defining for each combination an overall coefficient of linear correlation obtained as arithmetic mean of the quantized values associated to the sub-intervals containing a number of coefficient greater than 50%.

Claim 9 (Withdrawn): The method of claim 5, comprising
calculating coefficients of quadratic correlation of all pairs of gene sequences of a same combination;

defining for each combination a global coefficient of quadratic correlation obtained as an arithmetic mean of said correlation values.

Claim 10 (Withdrawn): The method of claim 5, comprising
calculating a percentage of gene sequences of the pair combination with a final value of gene expression greater than the initial value of gene expression;

defining a coefficient of global variation of the value of gene expression, comprised between 0 and 1, corresponding to said percentage.

Claim 11 (Withdrawn): The method of claim 5, comprising
calculating a percentage of gene sequences of the pair combination with an increasing time evolution;

defining a coefficient relative to the time evolution of the gene expression comprised between 0 and 1 corresponding to said percentage.

Claim 12 (Withdrawn): The method of claim 5, comprising
calculating a percentage of gene sequences of the pair combination with a value of gene expression greater than a pre-established threshold in correspondence of a same instant;

defining a coefficient of presence of maximum excursion of the level of gene expression in correspondence of the same instant, comprised between 0 and 1, corresponding to said percentage.

Claim 13 (Currently Amended): An identification computer system of groups of co-expressed and co-regulated genes, comprising:

a pre-processing sub-system input with data of a table relative to gene expressions variable with time and/or different environmental conditions, the pre-processing sub-system connected to a computer readable medium having executable instructions for generating sub-tables of data in groups of genes that satisfy a pre-established clustering criterion;

a processing sub-system of data of said sub-tables, the processing sub-system connected to a computer readable medium having executable instructions for considering all possible pairs of generated sub-tables and generating signals, for each pair of sub-tables, representing characteristic parameters of data associated to genes of that pair of sub-tables which express correlation among and between the included genes; and

an intelligent sub-system input with said signals representative of characteristic parameters, connected to a computer readable medium having executable instructions for generating for each pair of sub-tables a characteristic value determined as a function of the characteristic parameters and outputting to a user the groups of genes within each pair of sub-tables whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes involved in a particular cellular process.

Claim 14 (Currently Amended):The computer system of claim 13, wherein said intelligent sub-system is a neural fuzzy logic sub-system, trained off-line.

Claim 15 (Currently Amended):A computer program product embodied on a computer readable medium that executes a method for identifying groups of co-regulated and co-expressed genes, the method comprising:

receiving a table of data relating to evolution of gene expression with time and/or with changing environmental conditions for a plurality of genes;

applying a clustering algorithm to the table of data so as to identify clusters in the form of sub-tables comprising groups of genes that satisfy certain clustering criterion;

establishing all possible pair combinations of said clusters;

for each cluster pair combination, calculating a characteristic value for the cluster pair combination as a function of a plurality of characteristic parameters determined for each cluster pair which express a level of correlation which exists among and between the genes included in that cluster pair combination;

identifying the genes associated with cluster pair combinations whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes involved in a particular cellular process; and

outputting to a user the genes within the cluster pair combinations identified as being members of the network in a selected data format.

Claim 16 (Currently Amended): A computer program product embodied on a computer readable medium that executes a method for identifying groups of co-regulated and co-expressed genes, the method comprising:

receiving a table of data relating to evolution of gene expression with time and/or with changing environmental conditions for a plurality of genes;

applying a clustering algorithm to the table of data so as to identify clusters in the form of sub-tables comprising groups of genes that satisfy certain clustering criterion;

applying a filtering algorithm to the table of data so as to identify filter data in the form of sub-tables comprising groups of genes that satisfy certain filtering criteria;

establishing all possible pair combinations of said clusters, all possible pair combinations of filter data, and all possible pair combinations of clusters and filter data;

for each pair combination, calculating a characteristic value for the pair combination as a function of a plurality of characteristic parameters determined for each pair combination which express a level of correlation which exists among and between the genes included in that pair combination;

identifying the genes associated with pair combinations whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes involved in a particular cellular process; and

outputting to a user the genes within the pair combinations identified as being members of the network in a selected data format.

Claim 17 (Currently Amended): A computer program product embodied on a computer readable medium that executes a method for the identification of groups of co-expressed and co-regulated genes, the method comprising:

receiving data in table format relative to gene expressions which are variable with time and/or different environmental conditions;

generating sub-tables of data in groups of genes that satisfy a pre-established clustering criterion;

identifying all possible pairs of generated sub-tables;

generating signals, for each pair of sub-tables, representing characteristic parameters of data associated to genes of that pair of sub-tables which express correlation among and between the included genes;

processing said signals representative of characteristic parameters to generate for each pair of sub-tables a characteristic value determined as a function of the characteristic parameters;

identifying groups of genes from each pair of sub-tables whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes involved in a particular cellular process; and

outputting to a user data in a selected format including the groups of genes within each pair of sub-tables identified as being members of the network of genes.

Claim 18 (New): An integrated circuit implementing a method for identifying groups of co-regulated and co-expressed genes implemented on an integrate circuit, the method comprising:

defining a clustering criterion of data, relating to gene expression that varies with time and/or with the changing of environmental conditions, which is stored in a table;

in function of said clustering criterion, identifying in sub-tables groups of genes that satisfy said clustering criterion;

defining a number of logic filtering criteria of the data of said table;

for each logic filtering criterion, generating a corresponding filtered sub-table containing data of genes having expression values which satisfy said logic filtering criterion;

establishing pair combinations of said sub-tables by clustering and filtering the data of said table with said filtering criteria and by said clustering;

calculating characteristic parameters of the data associated to the groups of genes of each pair combination;

generating for each pair combination a characteristic value in function of the characteristic parameters of the groups of genes by a decision algorithm based on soft computing techniques;

identifying the groups of genes associated with pair combinations whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes involved in a particular cellular process and discarding pair combinations of groups of genes whose characteristic value is smaller than said threshold; and

outputting to a user the group of genes within the pair combinations having characteristic values greater than the threshold in a selected data format.

Claim 19 (New): An identification integrated circuit system of groups of co-expressed and co-regulated genes, comprising:

a pre-processing sub-system input with data of a table relative to gene expressions variable with time and/or different environmental conditions, the pre-processing sub-system implemented on an integrated circuit for generating sub-tables of data in groups of genes that satisfy a pre-established clustering criterion;

a processing sub-system of data of said sub-tables, the processing sub-system implemented on an integrated circuit for considering all possible pairs of generated sub-tables and generating signals, for each pair of sub-tables, representing characteristic parameters of data associated to genes of that pair of sub-tables which express correlation among and between the included genes; and

an intelligent sub-system input with said signals representative of characteristic parameters, implemented on an integrated circuit for generating for each pair of sub-tables a characteristic value determined as a function of the characteristic parameters and outputting to a user the groups of genes within each pair of sub-tables whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes involved in a particular cellular process.

Claim 20 (New): An integrated circuit implementing a method for identifying groups of co-regulated and co-expressed genes, the method comprising:

receiving a table of data relating to evolution of gene expression with time and/or with changing environmental conditions for a plurality of genes;

applying a clustering algorithm to the table of data so as to identify clusters in the form of sub-tables comprising groups of genes that satisfy certain clustering criterion;

establishing all possible pair combinations of said clusters;

for each cluster pair combination, calculating a characteristic value for the cluster pair combination as a function of a plurality of characteristic parameters determined for each cluster pair which express a level of correlation which exists among and between the genes included in that cluster pair combination;

identifying the genes associated with cluster pair combinations whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes involved in a particular cellular process; and

outputting to a user the genes within the cluster pair combinations identified as being members of the network in a selected data format.

Claim 21 (New): An integrated circuit implementing a method for identifying groups of co-regulated and co-expressed genes, the method comprising:

receiving a table of data relating to evolution of gene expression with time and/or with changing environmental conditions for a plurality of genes;

applying a clustering algorithm to the table of data so as to identify clusters in the form of sub-tables comprising groups of genes that satisfy certain clustering criterion;

applying a filtering algorithm to the table of data so as to identify filter data in the form of sub-tables comprising groups of genes that satisfy certain filtering criteria;

establishing all possible pair combinations of said clusters, all possible pair combinations of filter data, and all possible pair combinations of clusters and filter data;

for each pair combination, calculating a characteristic value for the pair combination as a function of a plurality of characteristic parameters determined for each pair combination which express a level of correlation which exists among and between the genes included in that pair combination;

identifying the genes associated with pair combinations whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes involved in a particular cellular process; and

outputting to a user the genes within the pair combinations identified as being members of the network in a selected data format.

Claim 22 (New): An integrated circuit implementing a method for the identification of groups of co-expressed and co-regulated genes, the method comprising:

receiving data in table format relative to gene expressions which are variable with time and/or different environmental conditions;

generating sub-tables of data in groups of genes that satisfy a pre-established clustering criterion;

identifying all possible pairs of generated sub-tables;

generating signals, for each pair of sub-tables, representing characteristic parameters of data associated to genes of that pair of sub-tables which express correlation among and between the included genes;

processing said signals representative of characteristic parameters to generate for each pair of sub-tables a characteristic value determined as a function of the characteristic parameters;

identifying groups of genes from each pair of sub-tables whose characteristic value is greater than a certain pre-established threshold as being members of a network of genes involved in a particular cellular process; and

outputting to a user data in a selected format including the groups of genes within each pair of sub-tables identified as being members of the network of genes.